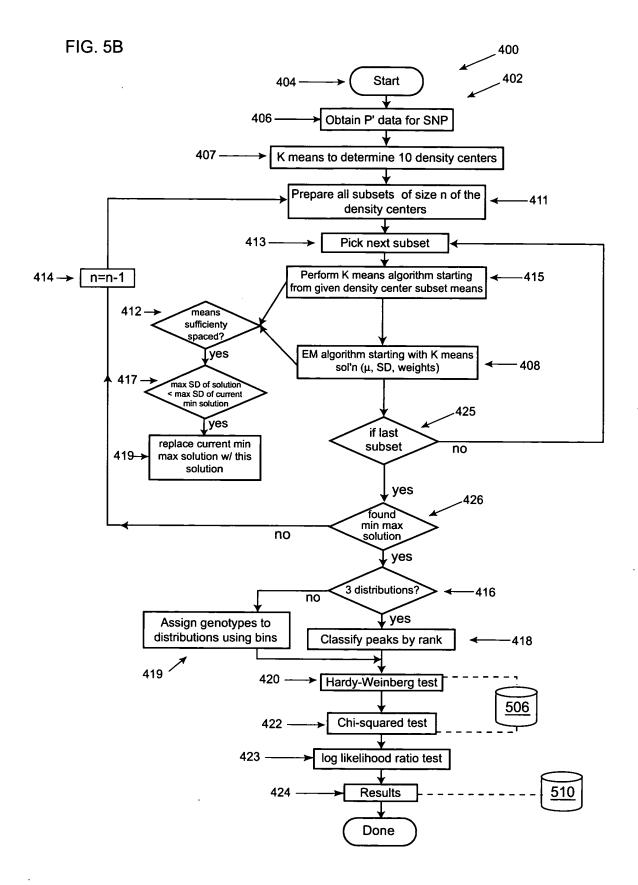


Fig. 5A



502 ----

EM_Genotyping_analysis

genotyping_analysis_id analysis_name genotyping_analysis_type description project_name created_dt analyzed_dt

EM_Genotyping_analysis_scan

genotpying_analysis_id scan_experiment_id

-504

500

506—-

EM_Genotype_snp_data

genotpying_analysis_id snp_id num_scans num_clusters final_log_likelihood hardy_weinberg_p_value min_chi2_p_value_0_05 EM_Genotype_cluster_data

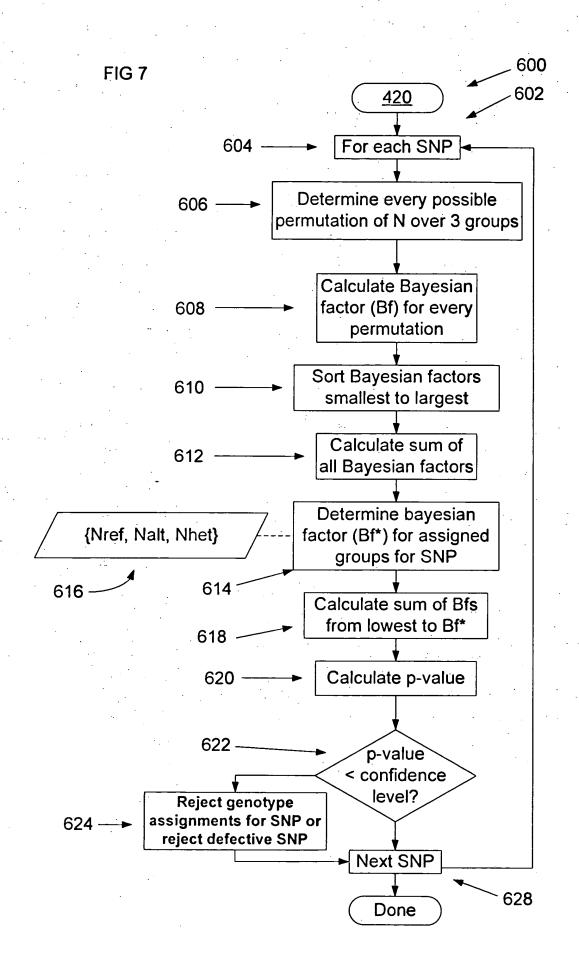
genotyping_analysis_id snp_id cluster_number mean standard_deviation weight assigned_genotype chi2_p_value_0_05

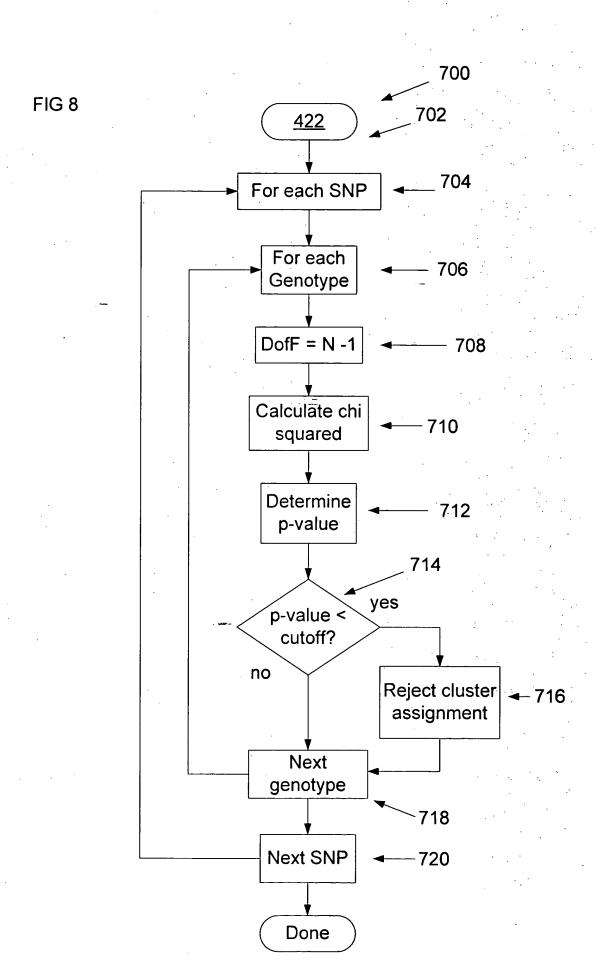
508

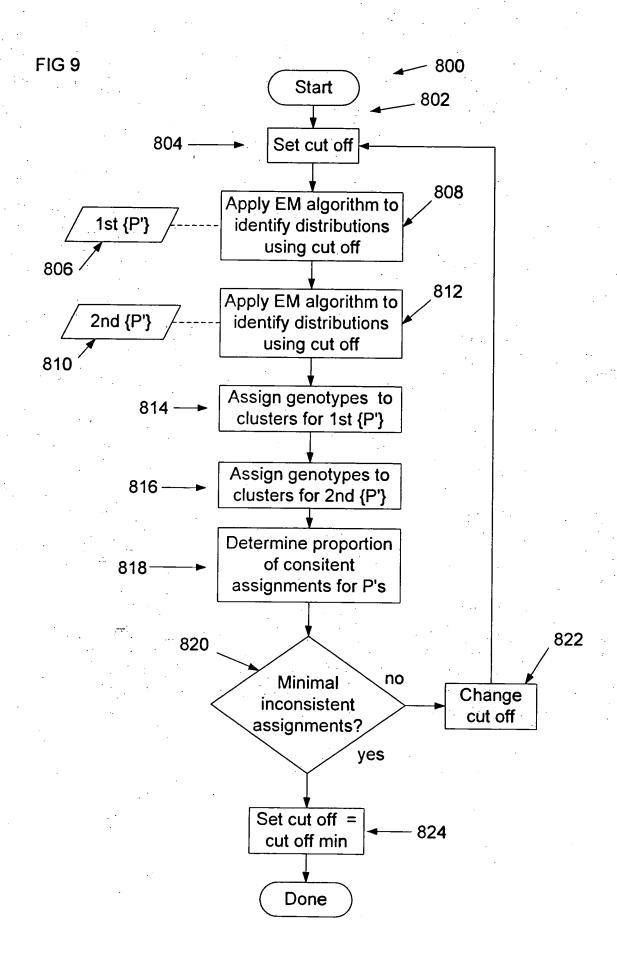
510 — **▶**

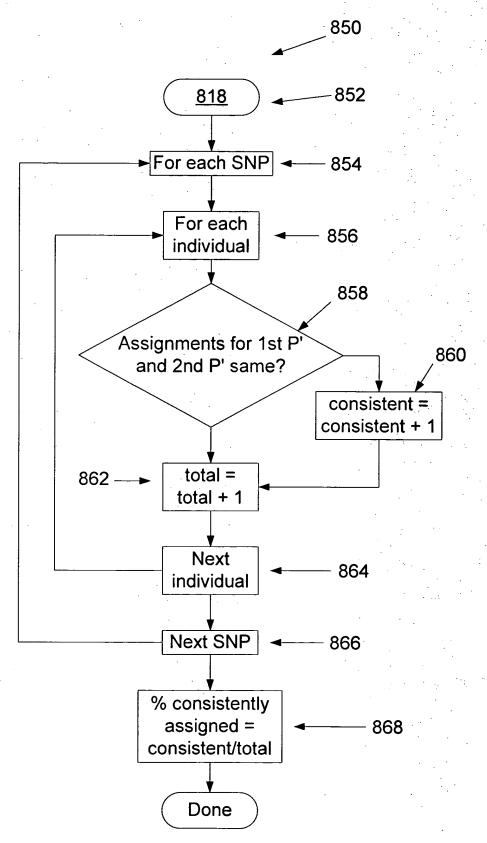
EM_snp_genotype

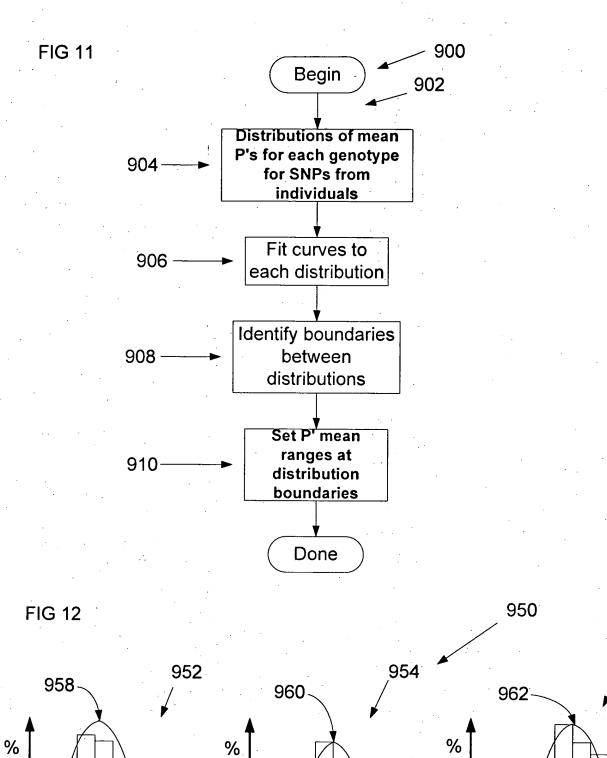
genotyping_analysis_id snp_design_block_id scan_experiment_id snp_id cluster_number cluster_log_likelihood next_max_log_likelihood_ratio











0.5

P'

0.24

P'

956

P'

0.76 0.5

FIG13A

